

#### RAW.SEQUENCE LISTING PATENT APPLICATION US/08/933,821

DATE: 12/22/97 TIME: 14:09:48

INPUT SET: S22244.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

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ENTERED
                                       SEQUENCE LISTING
1
 2
 3
    (1) General Information:
 4
 5
       (i) APPLICANT: Godowski, Paul J.
 6
                       Gurney, Austin L.
 7
 8
      (ii) TITLE OF INVENTION: Tie Ligands
 9
10
     (iii) NUMBER OF SEQUENCES: 17
11
      (iv) CORRESPONDENCE ADDRESS:
12
13
            (A) ADDRESSEE: Genentech, Inc.
14
            (B) STREET: 1 DNA Way
15
            (C) CITY: South San Francisco
16
            (D) STATE: California
            (E) COUNTRY: USA
17
18
            (F) ZIP: 94080
19
       (v) COMPUTER READABLE FORM:
20
            (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
21
            (B) COMPUTER: IBM PC compatible
22
23
            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24
            (D) SOFTWARE: WinPatin (Genentech)
25
      (vi) CURRENT APPLICATION DATA:
26
27
            (A) APPLICATION NUMBER:
28
            (B) FILING DATE:
29
            (C) CLASSIFICATION:
30
    (viii) ATTORNEY/AGENT INFORMATION:
31
32
            (A) NAME: Dreger, Ginger R.
            (B) REGISTRATION NUMBER: 33,055
33
34
            (C) REFERENCE/DOCKET NUMBER: P1130
35
36
      (ix) TELECOMMUNICATION INFORMATION:
            (A) TELEPHONE: 650/225-3216
37
38
            (B) TELEFAX: 650/952-9881
    (2) INFORMATION FOR SEQ ID NO:1:
39
40
41
        (i) SEQUENCE CHARACTERISTICS:
42
            (A) LENGTH: 2290 base pairs
43
            (B) TYPE: Nucleic Acid
44
            (C) STRANDEDNESS: Single
45
            (D) TOPOLOGY: Linear
46
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#### RAW SEQUENCE LISTING PATENT APPLICATION US/08/933,821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GGCTGAGGGG AGGCCCGGAG CCTTTCTGGG GCCTGGGGGA TCCTCTTGCA 50 CTGGTGGGTG GAGAGAGCG CCTGCAGCCA ACCAGGGTCA GGCTGTGCTC 100 ACAGTTTCCT CTGGCGGCAT GTAAAGGCTC CACAAAGGAG TTGGGAGTTC 150 AAATGAGGCT GCTGCGGACG GCCTGAGGAT GGACCCCAAG CCCTGGACCT 200 GCCGAGCGTG GCACTGAGGC AGCGGCTGAC GCTACTGTGA GGGAAAGAAG 250 GTTGTGAGCA GCCCGCAGG ACCCCTGGCC AGCCCTGGCC CCAGCCTCTG 300 CCGGAGCCCT CTGTGGAGGC AGAGCCAGTG GAGCCCAGTG AGGCAGGGCT 350 GCTTGGCAGC CACCGGCCTG CAACTCAGGA ACCCCTCCAG AGGCCATGGA 400 CAGGCTGCCC CGCTGACGC CAGGGTGAAG CATGTGAGGA GCCGCCCGG 450 AGCCAAGCAG GAGGGAAGAG GCTTTCATAG ATTCTATTCA CAAAGAATAA 500 CCACCATTTT GCAAGGACCA TGAGGCCACT GTGCGTGACA TGCTGGTGGC 550 TCGGACTGCT GGCTGCCATG GGAGCTGTTG CAGGCCAGGA GGACGGTTTT 600 GAGGGCACTG AGGAGGGCTC GCCAAGAGAG TTCATTTACC TAAACAGGTA 650 CAAGCGGGCG GGCGAGTCCC AGGACAAGTG CACCTACACC TTCATTGTGC 700 CCCAGCAGCG GGTCACGGGT GCCATCTGCG TCAACTCCAA GGAGCCTGAG 750 GTGCTTCTGG AGAACCGAGT GCATAAGCAG GAGCTAGAGC TGCTCAACAA 800 TGAGCTGCTC AAGCAGAAGC GGCAGATCGA GACGCTGCAG CAGCTGGTGG 850 AGGTGGACGG CGGCATTGTG AGCGAGGTGA AGCTGCTGCG CAAGGAGAGC 900 CGCAACATGA ACTCGCGGGT CACGCAGCTC TACATGCAGC TCCTGCACGA 950 GATCATCCGC AAGCGGGACA ACGCGTTGGA GCTCTCCCAG CTGGAGAACA 1000 GGATCCTGAA CCAGACAGCC GACATGCTGC AGCTGGCCAG CAAGTACAAG 1050 GACCTGGAGC ACAAGTACCA GCACCTGGCC ACACCGACCAATC 1100 AGAGATCATC GCGCAGCTTG AGGAGCACTG CCAGAGGGTG CCCTCGGCCA 1150 GGCCGTCCC CCAGCCACCC CCCGCTGCCC CGCCCCGGGT CTACCAACCA 1200 CCCACCTACA ACCGCATCAT CAACCAGATC TCTACCAACG AGATCCAGAG 1250

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					II.	
100 101	TGACCAGAAC	CTGAAGGTGC	TGCCACCCCC	TCTGCCCACT	ATGCCCACTC	1300
102	TCACCAGCCT	CCCATCTTCC	ACCGACAAGC	CGTCGGGCCC	ATGGAGAGAC	1350
103						
104 105	TGCCTGCAGG	CCCTGGAGGA	TGGCCACGAC	ACCAGCTCCA	TCTACCTGGT	1400
106	GNAGCCGGAG	AACACCAACC	<b>СССТСАТССА</b>	сстатастас	GACCAGAGAC	1450
107	GAAGCCGGAG	AACACCAACC	GCCTCATGCA	GGIGIGGIGC	GACCAGAGAC	1430
108	ACGACCCCGG	GGGCTGGACC	GTCATCCAGA	GACGCCTGGA	таастстатт	1500
109	noonoocoo	00001001.00	0101110011011	3	1000101011	1300
110	AACTTCTTCA	GGAACTGGGA	GACGTACAAG	CAAGGGTTTG	GGAACATTGA	1550
111						
112	CGGCGAATAC	TGGCTGGGCC	TGGAGAACAT	TTACTGGCTG	ACGAACCAAG	1600
113						
114	GCAACTACAA	ACTCCTGGTG	ACCATGGAGG	ACTGGTCCGG	CCGCAAAGTC	1650
115						
116	TTTGCAGAAT	ACGCCAGTTT	CCGCCTGGAA	CCTGAGAGCG	AGTATTATAA	1700
117						_,,,,
118	GCTGCGGCTG	GGGCGCTACC	ATGGCAATGC	GGGTGACTCC	TTTACATGGC	1750
119						
120	ACAACGGCAA	GCAGTTCACC	ACCCTGGACA	GAGATCATGA	TGTCTACACA	1800
121						2000
122	GGAAACTGTG	CCCACTACCA	GAAGGGAGGC	ТССТССТАТА	ACCCCTCTCC	1850
123						
124	CCACTCCAAC	CTCAACGGGG	TCTGGTACCG	CGGGGGCCAT	TACCGGAGCC	1900
125						
126	GCTACCAGGA	CGGAGTCTAC	TGGGCTGAGT	TCCGAGGAGG	CTCTTACTCA	1950
127						
128	CTCAAGAAAG	TGGTGATGAT	GATCCGACCG	AACCCCAACA	CCTTCCACTA	2000
129						
130	AGCCAGCTCC	CCCTCCTGAC	CTCTCGTGGC	CATTGCCAGG	AGCCCACCCT	2050
131						
132	GGTCACGCTG	GCCACAGCAC	AAAGAACAAC	TCCTCACCAG	TTCATCCTGA	2100
133						
134	GGCTGGGAGG	ACCGGGATGC	TGGATTCTGT	TTTCCGAAGT	CACTGCAGCG	2150
135						
136	GATGATGGAA	CTGAATCGAT	ACGGTGTTTT	CTGTCCCTCC	TACTTTCCTT	2200
137						
138	CACACCAGAC	AGCCCCTCAT	GTCTCCAGGA	CAGGACAGGA	CTACAGACAA	2250
139						
140	CTCTTTCTTT	AAATAAATTA	AGTCTCTACA	ATAAAAAAA	2290	
141						
142	(2) INFORMA	TION FOR SEC	Q ID NO:2:			
143						
144	(i) SEQU	ENCE CHARACT	TERISTICS:			
145	(A)	LENGTH: 493	amino acida	3		
146	(B)	TYPE: Amino	Acid			
147	(D)	TOPOLOGY: L:	inear			
148						
149	· (xi) SEQU	ENCE DESCRI	PTION: SEQ	ID NO:2:		
150						
151	Met Arg Pr	o Leu Cys Va	al Thr Cys '	Trp Trp Leu	Gly Leu Leu	ı Ala
152	1	5		10		15

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														INI	OT S
153 154 155 156	Ala	Met	Gly	Ala	Val 20	Ala	Gly	Gln	Glu	Asp 25	Gly	Phe	Glu	Gly	Thr 30
157 158 159	Glu	Glu	Gly	Ser	Pro 35	Arg	Glu	Phe	Ile	Tyr 40	Leu	Asn	Arg	Tyr	Lys 45
160 161 162	Arg	Ala	Gly	Glu	Ser 50	Gln	Asp	Lys	Cys	Thr 55	Tyr	Thr	Phe	Ile	Val 60
163 164 165	Pro	Gln	Gln	Arg	Val 65	Thr	Gly	Ala	Ile	Cys 70	Val	Asn	Ser	Lys	Glu 75
166 167 168	Pro	Glu	Val	Leu	Leu 80	Glu	Asn	Arg	Val	His 85	Lys	Gln	Glu	Leu	Glu 90
169 170 171	Leu	Leu	Asn	Asn	Glu 95	Leu	Leu	Lys	Gln	Lys 100	Arg	Gln	Ile	Glu	Thr 105
172 173 174	Leu	Gln	Gln	Leu	Val 110	Glu	Val	Asp	Gly	Gly 115	Ile	Val	Ser	Glu	Val 120
175 176 177	Lys	Leu	Leu	Arg	Lys 125	Glu	Ser	Arg	Asn	Met 130	Asn	Ser	Arg	Val	Thr 135
178 179 180	Gln	Leu	Tyr	Met	Gln 140	Leu	Leu	His	Glu	Ile 145	Ile	Arg	Lys	Arg	Asp 150
181 182 183			·		Leu 155					160					165
184 185 186	Thr	Ala	Asp	Met	Leu 170	Gln	Leu	Ala	Ser	Lys 175	Tyr	Lys	Asp	Leu	Glu 180
187 188 189	His	Lys	Tyr	Gln	His 185	Leu	Ala	Thr	Leu	Ala 190	His	Asn	Gln	Ser	Glu 195
190 191 192					Leu 200				_	205					210
193 194 195					Gln 215					220			_		225
196 197 198					230					235					Asn 240
199 200 201					245				-	250					Leu 255
202 203 204					Thr 260					265					270
205	Pro	Ser	Gly	Pro	Trp	Arg	Asp	Cys	Leu	Gln	Ala	Leu	Glu	Asp	Gly

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206					275					280	,			INI	PUT SET: S22244.raw 285
207 208 209 210	His	Asp	Thr	Ser	Ser 290	Ile	Tyr	Leu	Val	Lys 295	Pro	Glu	Asn	Thr	Asn 300
211 212 213	Arg	Leu	Met	Gln	Val 305	Trp	Cys	Asp	Gln	Arg 310	His	Asp	Pro	Gly	Gly 315
214 215 216	Trp	Thr	Val	Ile	Gln 320	Arg	Arg	Leu	Asp	Gly 325	Ser	Val	Asn	Phe	Phe 330
217 218 219	Arg	Asn	Trp	Glu	Thr 335	Tyr	Lys	Gln-	Gly	Phe 340	Gly	Asn	Ile	Asp	Gly 345
220 221 222	Glu	Tyr	Trp	Leu	Gly 350	Leu	Glu	Asn	Ile	Tyr 355	Trp	Leu	Thr	Asn	Gln 360
223 224 225	_		-	Lys	365					370	_			_	375
226 227 228	-			Ala	380	-				385					390
229 230 231		-	-	Lys 	395	_		-	_	400		_			405
232 233 234	_			Thr	410			-	_	415					420
235 236 237	J	_		Asp	425	-		_		430			_		435
238 239 240 241	_	_	_	Trp	440			_	•	445					450
241 242 243 244		_	_	Ala	455	_		_		460		_		_	465
245 246 247		_	_	Met	470		_		_	475	_			БуБ	480
248 249 250				-	485					490	****		493		
250 (2) INFORMATION FOR SEQ ID NO:3: 251 252 (i) SEQUENCE CHARACTERISTICS: 253 (A) LENGTH: 3355 base pairs 254 (B) TYPE: Nucleic Acid 255 (C) STRANDEDNESS: Single 256 (D) TOPOLOGY: Linear 257 258 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:															
200	( 1.	_ , 5.	- 2 - 11	1				~-~	1		-				

## SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/933,821

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Original Text